STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 11035, 377

Source: 1-14-05   iFWO

Date Processed by STIC: 2-2-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
    http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: *11/035,377*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response - ·· — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

This is a NON-ASCII text file, pls see item #4 on error summary sheet.

PAGE 1

SEQUENCE LISTING

Invalid numeric identifier →

Applicant info. is inserted at numeric identifier <110>

<100> EP Hoffman et al, Dkt. No. 64688/157

<120> - please insert title of invention → more to

<130> insert here

pls insert: →

<200> SEQUENCE CHARACTERISTICS — delete

<210> SEQ ID NO.1 (-G171T) — move to section <220>-<223>.

<1407 current application #

<1417 current filing date

<1607 # of seq ID #s

<1707 software type

delete, pls do not insert numeric identifiers.

<211> 60

<212> DNA

<213> Homo sapiens

<2037 <313> Allele G/T — This response is to be inserted into <220>-<223>.

<400> 1

pls use "K"

CCCAGGAGGT TTTTG[G/T]GCTT GCCTGGAGGG CCCAGGAGGT
TTTTGGCTTG CGCTGGAGGG

pls use lower CAPS

<200> SEQUENCE CHARACTERISTICS — delete

<210> SEQ ID NO.2 (-C8541T) — move to section <220>-<223>.

pls do not insert numeric identifiers.

<211> (62) 61

<212> DNA

<213> Homo sapiens

<313> Allele C/T — Insert into section <220>-<223>.

Invalid numeric identifier.

<400> 2

pls use "Y"

GCCAGACTT CAACGA[C/T]AGG TCCAGGGCCT GG

GCCAGACT TCAACGAAGG TCCAGGGCCT GG ← pls use lower CAPS

<200> SEQUENCE CHARACTERISTICS — delete

pls do not use numeric identifiers

<210> SEQ ID NO.3 (-C12273A) — Insert into section <220>-<223>.

<211> 61

<212> DNA

<213> Homo sapiens — Insert into section <220>-<223>.

<313> Allele C/T — Insert into section <220>-<223>.

Invalid numeric identifier

<400> 3

pls use "H"

CCCTGCAGGA CAGGG[C/A]ACTG GTCCAAACTC ACCCTGCAGG

ACAGGGACTG GTCCAAACTC A

pls use lower CAPS

Pls see the (Attached) sample sequence listing.

EVI: pls group Nucleotides in sets of tens. For example: aatcgaaggt

Certification

The undersigned certifies that the SEQUENCING LISTING shown above is exactly the same as that appearing in the paper patent application.

/Dr. Melvin Blecher/   01/03/2004
Reg. No. 33,649
Attorney for Applicant

1 pls delete

(Sample sequence listing)

<110>	Smith, John; Smithgene Inc.					

<120>   Example of a Sequence Listing

<130>   01-00001

<140>   PCT/EP98/00001
<141>   1998-12-31

<150>   US 08/999,999
<151>   1997-10-15

<160>   4

<170>   PatentIn version 2.0

<210>   1
<211>   389
<212>   DNA
<213>   Paramecium sp.

<220>
<221>   CDS
<222>   (279)...(389)

<300>
<301>   Doe, Richard
<302>   Isolation and Characterization of a Gene Encoding a
          Protease from Paramecium sp.
<303>   Journal of Genes
<304>   1
<305>   4
<306>   1-7
<307>   1988-06-31
<308>   123456
<309>   1988-06-31

<400>   1

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agctgtagtc   attcctgtgt   cctcttctct   ctgggcttct   caccctgcta   atcagatctc        60

agggagagtg   tcttgaccct   cctctgcctt   tgcagcttca   caggcaggca   ggcaggcagc       120

tgatgtggca   attgctggca   gtgccacagg   cttttcagcc   aggcttaggg   tgggttccgc       180

cgcggcgcgg   cggcccctct   cgcgctcctc   tcgcgcctct   ctctcgctct   cctctcgctc       240
```

```
ggacctgatt   aggtgagcag   gaggaggggg   cagttagc        atg  gtt  tca  atg  ttc  agc  296
                                                        Met  Val  Ser  Met  Phe  Ser
                                                         1                    5


ttg  tct  ttc  aaa  tgg  cct  gga  ttt  tgt  ttg  ttt  gtt  tgt  ttg  ttc  caa  344
Leu  Ser  Phe  Lys  Trp  Pro  Gly  Phe  Cys  Leu  Phe  Val  Cys  Leu  Phe  Gln
               10                  15                       20


tgt  ccc  aaa  gtc  ctc  ccc  tgt  cac  tca  tca  ctg  cag  ccg  aat  ctt     389
Cys  Pro  Lys  Val  Leu  Pro  Cys  His  Ser  Ser  Leu  Gln  Pro  Asn  Leu
               25                  30                       35
```

<210>   2
<211>   37
<212>   PRT
<213>   Paramecium sp.

<400>   2
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Met  Val  Ser  Met  Phe  Ser  Leu  Ser  Phe  Lys  Trp  Pro  Gly  Phe  Cys  Leu
 1                    5                  10                      15


Phe  Val  Cys  Leu  Phe  Gln  Cys  Pro  Lys  Val  Leu  Pro  Cys  His  Ser  Ser
               20                  25                      30


Leu  Gln  Pro  Asn  Leu
               35
```

<210>   3
<211>   11
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Designed peptide based on size and polarity to act as a
         linker between the alpha and beta chains of Protein XYZ.

<400>   3
```
Met  Val  Asn  Leu  Glu  Pro  Met  His  Thr  Glu  Ile
 1                    5                  10
```

<210>   4
<400>   4
000